



SEQUENCE LISTING

<110> Skeiky, Yasir
Guderian, Jeffrey
Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding
Sequence to Facilitate Stable and High Yield Expression
of Heterologous Proteins

<130> 014058-008010US

<140> US 09/684,215

<141> 2000-10-06

<150> US 60/158,585

<151> 1999-10-07

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 32 KD serine protease MTB32A

<220>

<221> CDS

<222> (89)..(1156)

<223> MTB32A

<220>

<221> sig_peptide

<222> (89)..(184)

<223> N-terminal hydrophobic secretory signal sequence

<220>

<221> mat_peptide

<222> (185)..(1153)

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Met Ser Asn Ser Arg Arg Arg Ser
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ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
-20 -15 -10

ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208
Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
-5 -1 1 5

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| cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc | 256 |
| Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val | |
| 10 15 20 | |
| gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac | 304 |
| Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr | |
| 25 30 35 40 | |
| aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt | 352 |
| Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly | |
| 45 50 55 | |
| gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat | 400 |
| Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn | |
| 60 65 70 | |
| gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg | 448 |
| Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly | |
| 75 80 85 | |
| tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt | 496 |
| Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly | |
| 90 95 100 | |
| ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc | 544 |
| Gly Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro | |
| 105 110 115 120 | |
| gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg | 592 |
| Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala | |
| 125 130 135 | |
| gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat | 640 |
| Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp | |
| 140 145 150 | |
| tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat | 688 |
| Ser Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp | |
| 155 160 165 | |
| gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta | 736 |
| Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu | |
| 170 175 180 | |
| gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg | 784 |
| Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu | |
| 185 190 195 200 | |
| tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg | 832 |
| Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala | |
| 205 210 215 | |
| atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc | 880 |
| Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile | |
| 220 225 230 | |
| ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac | 928 |
| Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn | |
| 235 240 245 | |

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc 976
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 250 255 260

ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc 1024
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 265 270 275 280

aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt 1072
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 285 290 295

gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 1120
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
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ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgctcgcg 1166
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 315 320

gataccaccc gccggccggc caattggatt ggccgagcc gtgattgccg cgtgagcccc 1226
 cgagttccgt ctcccgtagc cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286
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 ggtttcagga gtcccgcgc gaccagacg gaccgtacgg tgactattac gtgtggagcg 1766
 acaccagcga gcgctacacc gacgccgga tcattctcgt cgacaccgaa gagtcgaact 1826
 ggatcattcga tcctgtccgc cgacagttct actggcaccg attctt 1872

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 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> 32 KD serine protease MTB32A

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 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
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 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
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<211> 396

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 14 KD C-terminal fragment of MTB32A Ra12

<220>

<221> CDS

<222> (1)..(396)

<223> Ra12

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48

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gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg   96
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
      20                      25                      30

ggg ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc   144
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35                      40                      45

ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg   192
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
      50                      55                      60

gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg   240
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
      65                      70                      75                      80

atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg   288
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85                      90                      95

gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg   336
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
      100                     105                     110

caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag   384
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
      115                     120                     125

gga ccc ccg gcc
Gly Pro Pro Ala
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<210> 4
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 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

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      20      25      30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35      40      45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
      50      55      60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
      65      70      75      80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85      90      95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
      100     105     110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
      115     120     125
Gly Pro Pro Ala
      130

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<210> 5
 <211> 702
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ral2-DPPD fusion
 polypeptide

<220>
 <221> CDS
 <222> (4)..(696)
 <223> Ral2-DPPD fusion polypeptide

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ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
                20             25             30

gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
                35             40             45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
    50             55             60

aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
    65             70             75

ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
    80             85             90             95

atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
                100             105             110

ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
                115             120             125

aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc gac gac 432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp
                130             135             140

gac gac aag gat cca cct gac ccg cat cag ccg gac atg acg aaa ggc 480
Asp Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly
    145             150             155

tat tgc ccg ggt ggc cga tgg ggt ttt ggc gac ttg gcc gtg tgc gac 528
Tyr Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp
    160             165             170             175

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ggc gag aag tac ccc gac ggc tcg ttt tgg cac cag tgg atg caa acg 576
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180 185 190

tgg ttt acc ggc cca cag ttt tac ttc gat tgt gtc agc ggc ggt gag 624
Trp Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu
195 200 205

ccc ctc ccc ggc ccg ccg cca ccg ggt ggt tgc ggt ggg gca att ccg 672
Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro
210 215 220

tcc gag cag ccc aac gct ccc tga gaattc 702
Ser Glu Gln Pro Asn Ala Pro
225 230

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<210> 6
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12-DPPD fusion
 polypeptide

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20 25 30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
35 40 45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
130 135 140
Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
145 150 155 160
Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
165 170 175
Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
180 185 190
Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
195 200 205
Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser
210 215 220
Glu Gln Pro Asn Ala Pro
225 230

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<210> 7
 <211> 1746
 <212> DNA
 <213> Artificial Sequence

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<220>
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 <222> (4)..(1740)
 <223> Ra12-WT1 fusion polypeptide

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 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
 20 25 30
 gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
 35 40 45
 atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
 Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
 50 55 60
 aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
 Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
 65 70 75
 ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
 Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
 80 85 90 95
 atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
 Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
 100 105 110
 ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
 Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
 115 120 125
 aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc ccg ctg 432
 Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu
 130 135 140
 gtg ccg cgc ggc agc ccg atg ggc tcc gac gtt cgg gac ctg aac gca 480
 Val Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala
 145 150 155
 ctg ctg ccg gca gtt ccg tcc ctg ggt ggt ggt ggt ggt tgc gca ctg 528
 Leu Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu
 160 165 170 175
 ccg gtt agc ggt gca gca cag tgg gct ccg gtt ctg gac ttc gca ccg 576
 Pro Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro
 180 185 190

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| ccg ggt gca tcc gca tac ggt tcc ctg ggt ggt ccg gca ccg ccg ccg Pro Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro | 624 |
| 195 200 205 | |
| gca ccg ccg ccg ccg ccg ccg ccg ccg ccg ccg cac tcc ttc atc aaa cag Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln | 672 |
| 210 215 220 | |
| gaa ccg agc tgg ggt ggt gca gaa ccg cac gaa gaa cag tgc ctg agc Glu Pro Ser Trp Gly Gly Ala Glu Pro His Glu Gln Cys Leu Ser | 720 |
| 225 230 235 | |
| gca ttc acc gtt cac ttc tcc ggc cag ttc act ggc aca gcc gga gcc Ala Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala | 768 |
| 240 245 250 255 | |
| tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag gcg tca tcc Cys Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser | 816 |
| 260 265 270 | |
| ggc cag gcc agg atg ttt cct aac gcg ccc tac ctg ccc agc tgc ctc Gly Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu | 864 |
| 275 280 285 | |
| gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe | 912 |
| 290 295 300 | |
| gac ggg acg ccc agc tac ggt cac acg ccc tcg cac cat gcg gcg cag Asp Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln | 960 |
| 305 310 315 | |
| ttc ccc aac cac tca ttc aag cat gag gat ccc atg ggc cag cag ggc Phe Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly | 1008 |
| 320 325 330 335 | |
| tcg ctg ggt gag cag cag tac tcg gtg ccg ccc ccg gtc tat ggc tgc Ser Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys | 1056 |
| 340 345 350 | |
| cac acc ccc acc gac agc tgc acc ggc agc cag gct ttg ctg ctg agg His Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg | 1104 |
| 355 360 365 | |
| acg ccc tac agc agt gac aat tta tac caa atg aca tcc cag ctt gaa Thr Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu | 1152 |
| 370 375 380 | |
| tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His | 1200 |
| 385 390 395 | |
| agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly | 1248 |
| 400 405 410 415 | |
| gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp | 1296 |
| 420 425 430 | |

| | |
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| gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cgg tcg gca tct | 1344 |
| Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser | |
| 435 440 445 | |
| gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat | 1392 |
| Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn | |
| 450 455 460 | |
| aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac | 1440 |
| Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His | |
| 465 470 475 | |
| act ggt gag aaa cca tac cag tgt gac ttc aag gac tgt gaa cga agg | 1488 |
| Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg | |
| 480 485 490 495 | |
| ttt ttt cgt tca gac cag ctc aaa aga cac caa agg aga cat aca ggt | 1536 |
| Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly | |
| 500 505 510 | |
| gtg aaa cca ttc cag tgt aaa act tgt cag cga aag ttc tcc cgg tcc | 1584 |
| Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser | |
| 515 520 525 | |
| gac cac ctg aag acc cac acc agg act cat aca ggt gaa aag ccc ttc | 1632 |
| Asp His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe | |
| 530 535 540 | |
| agc tgt cgg tgg cca agt tgt cag aaa aag ttt gcc cgg tca gat gaa | 1680 |
| Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu | |
| 545 550 555 | |
| tta gtc cgc cat cac aac atg cat cag aga aac atg acc aaa ctc cag | 1728 |
| Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln | |
| 560 565 570 575 | |
| ctg gcg ctt tga gaattc | 1746 |
| Leu Ala Leu | |

<210> 8
 <211> 578
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ral2-WT1 fusion polypeptide

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| 20 25 30 | |
| Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile | |
| 35 40 45 | |
| Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn | |
| 50 55 60 | |
| Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu | |
| 65 70 75 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ile | Ser | Thr | Gly | Asp | Val | Ile | Thr | Ala | Val | Asp | Gly | Ala | Pro | Ile | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Asn | Ser | Ala | Thr | Ala | Met | Ala | Asp | Ala | Leu | Asn | Gly | His | His | Pro | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Asp | Val | Ile | Ser | Val | Thr | Trp | Gln | Thr | Lys | Ser | Gly | Gly | Thr | Arg | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Gly | Asn | Val | Thr | Leu | Ala | Glu | Gly | Pro | Pro | Ala | Glu | Phe | Pro | Leu | Val | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Pro | Arg | Gly | Ser | Pro | Met | Gly | Ser | Asp | Val | Arg | Asp | Leu | Asn | Ala | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Leu | Pro | Ala | Val | Pro | Ser | Leu | Gly | Gly | Gly | Gly | Gly | Cys | Ala | Leu | Pro | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Val | Ser | Gly | Ala | Ala | Gln | Trp | Ala | Pro | Val | Leu | Asp | Phe | Ala | Pro | Pro | |
| | | | 180 | | | | 185 | | | | | | 190 | | | |
| Gly | Ala | Ser | Ala | Tyr | Gly | Ser | Leu | Gly | Gly | Pro | Ala | Pro | Pro | Pro | Ala | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | His | Ser | Phe | Ile | Lys | Gln | Glu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Ser | Trp | Gly | Gly | Ala | Glu | Pro | His | Glu | Glu | Gln | Cys | Leu | Ser | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Phe | Thr | Val | His | Phe | Ser | Gly | Gln | Phe | Thr | Gly | Thr | Ala | Gly | Ala | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Arg | Tyr | Gly | Pro | Phe | Gly | Pro | Pro | Pro | Pro | Ser | Gln | Ala | Ser | Ser | Gly | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Gln | Ala | Arg | Met | Phe | Pro | Asn | Ala | Pro | Tyr | Leu | Pro | Ser | Cys | Leu | Glu | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ser | Gln | Pro | Ala | Ile | Arg | Asn | Gln | Gly | Tyr | Ser | Thr | Val | Thr | Phe | Asp | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Gly | Thr | Pro | Ser | Tyr | Gly | His | Thr | Pro | Ser | His | His | Ala | Ala | Gln | Phe | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Pro | Asn | His | Ser | Phe | Lys | His | Glu | Asp | Pro | Met | Gly | Gln | Gln | Gly | Ser | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Leu | Gly | Glu | Gln | Gln | Tyr | Ser | Val | Pro | Pro | Pro | Val | Tyr | Gly | Cys | His | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Thr | Pro | Thr | Asp | Ser | Cys | Thr | Gly | Ser | Gln | Ala | Leu | Leu | Leu | Arg | Thr | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Pro | Tyr | Ser | Ser | Asp | Asn | Leu | Tyr | Gln | Met | Thr | Ser | Gln | Leu | Glu | Cys | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Met | Thr | Trp | Asn | Gln | Met | Asn | Leu | Gly | Ala | Thr | Leu | Lys | Gly | His | Ser | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Thr | Gly | Tyr | Glu | Ser | Asp | Asn | His | Thr | Thr | Pro | Ile | Leu | Cys | Gly | Ala | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Gln | Tyr | Arg | Ile | His | Thr | His | Gly | Val | Phe | Arg | Gly | Ile | Gln | Asp | Val | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Arg | Arg | Val | Pro | Gly | Val | Ala | Pro | Thr | Leu | Val | Arg | Ser | Ala | Ser | Glu | |
| | | 435 | | | | | | 440 | | | | 445 | | | | |
| Thr | Ser | Glu | Lys | Arg | Pro | Phe | Met | Cys | Ala | Tyr | Ser | Gly | Cys | Asn | Lys | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Arg | Tyr | Phe | Lys | Leu | Ser | His | Leu | Gln | Met | His | Ser | Arg | Lys | His | Thr | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Gly | Glu | Lys | Pro | Tyr | Gln | Cys | Asp | Phe | Lys | Asp | Cys | Glu | Arg | Arg | Phe | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Phe | Arg | Ser | Asp | Gln | Leu | Lys | Arg | His | Gln | Arg | Arg | His | Thr | Gly | Val | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| Lys | Pro | Phe | Gln | Cys | Lys | Thr | Cys | Gln | Arg | Lys | Phe | Ser | Arg | Ser | Asp | |
| | | 515 | | | | | | 520 | | | | 525 | | | | |
| His | Leu | Lys | Thr | His | Thr | Arg | Thr | His | Thr | Gly | Glu | Lys | Pro | Phe | Ser | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| Cys | Arg | Trp | Pro | Ser | Cys | Gln | Lys | Lys | Phe | Ala | Arg | Ser | Asp | Glu | Leu | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |

Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu
565 570 575
Ala Leu

<210> 9
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion

<220>
<221> CDS
<222> (4)..(666)
<223> Ra12-human mammaglobin fusion polypeptide

<400> 9
cat atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag 48
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln
1 5 10 15
ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
20 25 30
gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
35 40 45
atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
50 55 60
aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
65 70 75
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
80 85 90 95
atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
100 105 110
ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
115 120 125
aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atc gag 432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu
130 135 140
gga agg ggc tct ggc tgc ccc tta ttg gag aat gtg att tcc aag aca 480
Gly Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
145 150 155

| | |
|-----------------------------------------------------------------|-----|
| atc aat cca caa gtg tct aag act gaa tac aaa gaa ctt ctt caa gag | 528 |
| Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu | |
| 160 165 170 175 | |
| | |
| ttc ata gac gac aat gcc act aca aat gcc ata gat gaa ttg aag gaa | 576 |
| Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu | |
| 180 185 190 | |
| | |
| tgt ttt ctt aac caa acg gat gaa act ctg agc aat gtt gag gtg ttt | 624 |
| Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe | |
| 195 200 205 | |
| | |
| atg caa tta ata tat gac agc agt ctt tgt gat tta ttt taa gaattc | 672 |
| Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe | |
| 210 215 220 | |

<210> 10

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion polypeptide

<400> 10

| | |
|-----------------------------------------------------------------|--|
| Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu | |
| 1 5 10 15 | |
| Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala | |
| 20 25 30 | |
| Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile | |
| 35 40 45 | |
| Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn | |
| 50 55 60 | |
| Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu | |
| 65 70 75 80 | |
| Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile | |
| 85 90 95 | |
| Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly | |
| 100 105 110 | |
| Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr | |
| 115 120 125 | |
| Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly | |
| 130 135 140 | |
| Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile | |
| 145 150 155 160 | |
| Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe | |
| 165 170 175 | |
| Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys | |
| 180 185 190 | |
| Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met | |
| 195 200 205 | |
| Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe | |
| 210 215 220 | |

<210> 11

<211> 2191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-H9-32A fusion
(Ra12-MTB39-MTB32A(N-ter) fusion)

<220>

<221> CDS

<222> (1)..(2190)

<223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

<400> 11

| | |
|-----------------------------------------------------------------|-----|
| atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag ctg | 48 |
| Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu | |
| 1 5 10 15 | |
| tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg | 96 |
| Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala | |
| 20 25 30 | |
| atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc | 144 |
| Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile | |
| 35 40 45 | |
| ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac | 192 |
| Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn | |
| 50 55 60 | |
| ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc | 240 |
| Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu | |
| 65 70 75 80 | |
| ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc | 288 |
| Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile | |
| 85 90 95 | |
| aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt | 336 |
| Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly | |
| 100 105 110 | |
| gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca | 384 |
| Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr | |
| 115 120 125 | |
| ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atg gtg gat | 432 |
| Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp | |
| 130 135 140 | |
| ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc | 480 |
| Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly | |
| 145 150 155 160 | |
| ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg | 528 |
| Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val | |
| 165 170 175 | |
| gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg | 576 |
| Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp | |
| 180 185 190 | |
| ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg | 624 |
| Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val | |
| 195 200 205 | |

| | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln 210 215 220 | 672 |
| gcc gag ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu 225 230 235 240 | 720 |
| acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt Thr Ala Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg 245 250 255 | 768 |
| gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr 260 265 270 | 816 |
| ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln 275 280 285 | 864 |
| gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr 290 295 300 | 912 |
| gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly 305 310 315 320 | 960 |
| ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala 325 330 335 | 1008 |
| gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu 340 345 350 | 1056 |
| gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu 355 360 365 | 1104 |
| tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser 370 375 380 | 1152 |
| atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr 385 390 395 400 | 1200 |
| aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala 405 410 415 | 1248 |
| cag gcc gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser 420 425 430 | 1296 |
| ctg ggc agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala 435 440 445 | 1344 |

| | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| aac ttg ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala 450 455 460 | 1392 |
| tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro 465 470 475 480 | 1440 |
| ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu 485 490 495 | 1488 |
| ggc ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu 500 505 510 | 1536 |
| agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser 515 520 525 | 1584 |
| ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe 530 535 540 | 1632 |
| gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln 545 550 555 560 | 1680 |
| gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn 565 570 575 | 1728 |
| gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val 580 585 590 | 1776 |
| ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe 595 600 605 | 1824 |
| agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp 610 615 620 | 1872 |
| cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu 625 630 635 640 | 1920 |
| ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val 645 650 655 | 1968 |
| gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro 660 665 670 | 2016 |
| ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat tcg ctg Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu 675 680 685 | 2064 |

acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg 2112
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700

atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag 2160
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720

gtg gtc ggt atg aac acg gcc gcg tcc tag g 2191
 Val Val Gly Met Asn Thr Ala Ala Ser
 725 730

<210> 12

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ral2-H9-32A fusion
 polypeptide (Ral2-MTB39-MTB32A(N-ter) fusion polypeptide)

<400> 12

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220
 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Thr
 290 295 300

| | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Leu | Leu | Pro | Phe | Glu | Glu | Ala | Pro | Glu | Met | Thr | Ser | Ala | Gly | 305 | | 310 | | 315 | | 320 |
| Gly | Leu | Leu | Glu | Gln | Ala | Ala | Ala | Val | Glu | Glu | Ala | Ser | Asp | Thr | Ala | | 325 | | 330 | | 335 | |
| Ala | Ala | Asn | Gln | Leu | Met | Asn | Asn | Val | Pro | Gln | Ala | Leu | Gln | Gln | Leu | | 340 | | 345 | | 350 | |
| Ala | Gln | Pro | Thr | Gln | Gly | Thr | Thr | Pro | Ser | Ser | Lys | Leu | Gly | Gly | Leu | | 355 | | 360 | | 365 | |
| Trp | Lys | Thr | Val | Ser | Pro | His | Arg | Ser | Pro | Ile | Ser | Asn | Met | Val | Ser | | 370 | | 375 | | 380 | |
| Met | Ala | Asn | Asn | His | Met | Ser | Met | Thr | Asn | Ser | Gly | Val | Ser | Met | Thr | | 385 | | 390 | | 395 | |
| Asn | Thr | Leu | Ser | Ser | Met | Leu | Lys | Gly | Phe | Ala | Pro | Ala | Ala | Ala | Ala | | 405 | | 410 | | 415 | |
| Gln | Ala | Val | Gln | Thr | Ala | Ala | Gln | Asn | Gly | Val | Arg | Ala | Met | Ser | Ser | | 420 | | 425 | | 430 | |
| Leu | Gly | Ser | Ser | Leu | Gly | Ser | Ser | Gly | Leu | Gly | Gly | Gly | Val | Ala | Ala | | 435 | | 440 | | 445 | |
| Asn | Leu | Gly | Arg | Ala | Ala | Ser | Val | Gly | Ser | Leu | Ser | Val | Pro | Gln | Ala | | 450 | | 455 | | 460 | |
| Trp | Ala | Ala | Ala | Asn | Gln | Ala | Val | Thr | Pro | Ala | Ala | Arg | Ala | Leu | Pro | | 465 | | 470 | | 475 | |
| Leu | Thr | Ser | Leu | Thr | Ser | Ala | Ala | Glu | Arg | Gly | Pro | Gly | Gln | Met | Leu | | 485 | | 490 | | 495 | |
| Gly | Gly | Leu | Pro | Val | Gly | Gln | Met | Gly | Ala | Arg | Ala | Gly | Gly | Gly | Leu | | 500 | | 505 | | 510 | |
| Ser | Gly | Val | Leu | Arg | Val | Pro | Pro | Arg | Pro | Tyr | Val | Met | Pro | His | Ser | | 515 | | 520 | | 525 | |
| Pro | Ala | Ala | Gly | Asp | Ile | Ala | Pro | Pro | Ala | Leu | Ser | Gln | Asp | Arg | Phe | | 530 | | 535 | | 540 | |
| Ala | Asp | Phe | Pro | Ala | Leu | Pro | Leu | Asp | Pro | Ser | Ala | Met | Val | Ala | Gln | | 545 | | 550 | | 555 | |
| Val | Gly | Pro | Gln | Val | Val | Asn | Ile | Asn | Thr | Lys | Leu | Gly | Tyr | Asn | Asn | | 565 | | 570 | | 575 | |
| Ala | Val | Gly | Ala | Gly | Thr | Gly | Ile | Val | Ile | Asp | Pro | Asn | Gly | Val | Val | | 580 | | 585 | | 590 | |
| Leu | Thr | Asn | Asn | His | Val | Ile | Ala | Gly | Ala | Thr | Asp | Ile | Asn | Ala | Phe | | 595 | | 600 | | 605 | |
| Ser | Val | Gly | Ser | Gly | Gln | Thr | Tyr | Gly | Val | Asp | Val | Val | Gly | Tyr | Asp | | 610 | | 615 | | 620 | |
| Arg | Thr | Gln | Asp | Val | Ala | Val | Leu | Gln | Leu | Arg | Gly | Ala | Gly | Gly | Leu | | 625 | | 630 | | 635 | |
| Pro | Ser | Ala | Ala | Ile | Gly | Gly | Gly | Val | Ala | Val | Gly | Glu | Pro | Val | Val | | 645 | | 650 | | 655 | |
| Ala | Met | Gly | Asn | Ser | Gly | Gly | Gln | Gly | Gly | Thr | Pro | Arg | Ala | Val | Pro | | 660 | | 665 | | 670 | |
| Gly | Arg | Val | Val | Ala | Leu | Gly | Gln | Thr | Val | Gln | Ala | Ser | Asp | Ser | Leu | | 675 | | 680 | | 685 | |
| Thr | Gly | Ala | Glu | Glu | Thr | Leu | Asn | Gly | Leu | Ile | Gln | Phe | Asp | Ala | Ala | | 690 | | 695 | | 700 | |
| Ile | Gln | Pro | Gly | Asp | Ser | Gly | Gly | Pro | Val | Val | Asn | Gly | Leu | Gly | Gln | | 705 | | 710 | | 715 | |
| Val | Val | Gly | Met | Asn | Thr | Ala | Ala | Ser | | | | | | | | | 725 | | | | | |

<210> 13

<211> 51

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR amplification of Ra12 C-terminal
 fragment of MTB32A

<400> 13
 caattacata tgcatacaca tcaccatcac acggccgcgt ccgataactt c 51

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer for PCR amplification of
 Ra12 C-terminal fragment of MTB32A

<400> 14
 ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 15
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer containing enterokinase
 recognition site for PCR amplification of DPPD
 mature secreted form

<400> 15
 caattagaat tcgacgacga cgacaaggat ccacctgacc cgcatacag 48

<210> 16
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer containing enterokinase
 recognition site for PCR amplification of DPPD
 mature secreted form

<400> 16
 caattagaat tctcagggag cgttgggctg etc 33

<210> 17
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(short)
 polypeptide

<400> 17
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 18
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(long)
 polypeptide

<400> 18
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
 20 25 30
 Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
 35 40 45
 Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
 50 55 60
 Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
 65 70 75 80
 Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
 85 90 95
 Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
 100 105 110
 Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 115 120 125

<210> 19
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer, HindIII site, for PCR
 amplification of human mammaglobin

<400> 19
 gcgaagctta tgaagttgct gatggctcctc atgc

34

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer, XhoI site, for PCR
 amplification of human mammaglobin

<400> 20
 cggctcgagt taaaataaat cacaaagact gctgtc

36

<210> 21
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
 Met His His His His His His
 1 5

<210> 22
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:enterokinase
 recognition site

<400> 22
 Asp Asp Asp Lys
 1

<210> 23
 <211> 128
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> positions 1-128 of Ra12

<400> 23
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125